09/266,935

* * * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 06:33:32 ON 21 NOV 2000

=> file biosis medline wpids uspat

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*** YOU HAVE NEW MAIL ***

=> s (PCR or polymerase chain reaction) and review

L1 5642 (PCR OR POLYMERASE CHAIN REACTION) AND REVIEW

=> s (PCR or polymerase chain reaction)/ti and review

L2 347 (PCR OR POLYMERASE CHAIN REACTION)/TI AND REVIEW

=> s l2 and amino acid?

L3 8 L2 AND AMINO ACID?

=> dup rem l3

PROCESSING COMPLETED FOR L3
L4 8 DUP REM L3 (0 DUPLICATES REMOVED)

=> d l4 bib abs 1-8

L4 ANSWER 1 OF 8 USPATFULL
AN 1999:166788 USPATFULL
TI Salmonella identification by the **polymerase chain reaction**
IN Olsen, John Elmerdahl, Elmekrogen 4, DK-3500 Vaerlos, Denmark
Aabo, Soren, Tokkerupvej 11, Tokkerup, DK-4320 Lejre, Denmark
Rossen, Lone, Roskilde, Denmark
Rasmussen, Ole Feldballe, Maaloev, Denmark
PA Olsen, John Elmerdahl, Vaerlos, Denmark (non-U.S. individual)
Bioteknologisk Institut, Lyngby, Denmark (non-U.S. corporation)
Aabo, Soren, Lejre, Denmark (non-U.S. individual)
PI US 6004747 19991221
WO 9500664 19950105
AI US 1996-564110 19960311 (8)
WO 1994-GB1316 19940617
19960311 PCT 371 date

PRAI GB 1993-12508 19930617
DT Utility
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce
LREP Testa, Hurwitz & Thibeault, LLP
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 1152
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides nucleic acid molecules for the detection and identification of Salmonella species, methods for detecting one or more Salmonella serotpes using the nucleic acid molecules of the invention as
probes or primers in DNA-based detection systems and kits for carrying out the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 2 OF 8 USPATFULL
AN 1998:134819 USPATFULL
TI In situ recombinant **PCR** within single cells
IN Embleton, Michael J., Nottingham, United Kingdom
Gorochov, Guy, Cambridge, United Kingdom
Jones, Peter T., Cambridge, United Kingdom
Winter, Gregory P., Cambridge, United Kingdom
PA Medical Research Council, England (non-U.S. corporation)
PI US 5830663 19981103
WO 9303151 19930218
AI US 1994-190199 19940713 (8)
WO 1992-GB1483 19920810
19940713 PCT 371 date
19940713 PCT 102(e) date
PRAI GB 1991-17352 19910810
GB 1992-12419 19920611
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Fredman, Jeffrey
LREP Cushman Darby & Cushman IP Group of Pillsbury Madison & Sutro
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 19 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 1925
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method of treating a heterogeneous population of cells to
link together copies of two or more nucleic acid sequences from at least
some of the cells, the arrangement being such that copies of the DNA sequences from an individual cell are preferentially linked in the vicinity of the nucleic acid from which the copies are derived. Also disclosed are recombinant proteins expressed by the method of the invention and kits for performing said method.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 8 USPATFULL
AN 1998:118970 USPATFULL
TI **Polymerase chain reaction**/restriction
fragment polymorphism method for the detection and typing of human papillomaviruses
IN Silverstein, Saul J., Irvington, NY, United States
Lungu, Octavian, New York, NY, United States
Wright, Jr., Thomas C., Irvington, NY, United States
PA The Trustees of Columbia University in the City of New York, New York, NY, United States (U.S. corporation)

AI US 1996-594600 19960131 (8)
PLI Continuation of Ser. No. US 1994-255561, filed on 8 Jun 1994, now patented, Pat. No. US 5543294 which is a continuation of Ser. No. US 1992-916940, filed on 20 Jul 1992 which is a continuation-in-part of Ser. No. US 1991-733109, filed on 19 Jul 1991, now abandoned
DT Utility
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Brusca, John S.
LREP White, John P.
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 2023
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides a method of typing a human papillomavirus in a patient infected by human papillomavirus which comprises: obtaining a sample containing DNA from the human papillomavirus to be typed; amplifying the L1 portion of the human papillomavirus DNA; treating the resulting amplified DNA with a plurality of predetermined restriction enzymes so as to produce restriction fragments; and analyzing the fragments so produces so as to type the human papillomavirus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 4 OF 8 USPATFULL
AN 97:24905 USPATFULL
TI **PCR** primers for detection of legionella species and methods for controlling visual intensity in hybridization assays
IN Picone, Teresa K.H., Benicia, CA, United States
McCallum, Theresa M., Pleasant Hill, CA, United States
Zoccoli, Michael A., Moraga, CA, United States
PA Hoffmann-La Roche Inc., Nutley, NJ, United States (U.S. corporation)
PI US 5614388 19970325
AI US 1995-455116 19950531 (8)
PLI Continuation of Ser. No. US 1993-70328, filed on 27 May 1993, now patented, Pat. No. US 5491225 which is a continuation-in-part of Ser. No. US 1990-630899, filed on 20 Dec 1990, now abandoned
DT Utility
EXNAM Primary Examiner: Sisson, Bradley L.
LREP Johnston, George W.; Sias, Stacey R.; Petry, Douglas A.
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1323
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides for superior nucleic acid primers for amplification of select target regions of the genome of the genus Legionella. The invention facilitates detection of pathogenic and nonpathogenic forms of this genus. The invention further provides for processes for using the primers in template dependent nucleic acid polymerase extension reactions to amplify select target regions. Kits for the use of these primers are also provided.

This invention further provides for methods of controlling the intensity
of visual signal for detection of duplex formation in nucleic acid hybridization assays under high stringent conditions. This method involves the blending of different capture probes onto a solid support.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 5 OF 8 USPATFULL
AN 96:70337 USPATFULL
TI **Polymerase chain reaction**/restriction
fragment length polymorphism method for the detection and typing of

IN Silverstein, Saul J., Irvington, NY, United States
Lungu, Octavian, New York, NY, United States
Wright, Jr., Thomas C., Irvington, NY, United States
PA The Trustees of Columbia University in the City of New York, New York, NY, United States (U.S. corporation)
PI US 5543294 19960806
AI US 1994-255561 19940608 (8)
PLI Continuation of Ser. No. US 1992-916940, filed on 20 Jul 1992, now abandoned which is a continuation-in-part of Ser. No. US 1991-733109, filed on 19 Jul 1991, now abandoned
DT Utility
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Brusca, John S.
LREP White, John P.
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1947
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The subject invention provides a method of diagnosing congenital adrenal hyperplasia in a human subject. The subject invention also provides a method of typing a human papillomavirus in a patient infected by a human papillomavirus. The subject invention further provides a method for detecting Mycobacteria in a clinical sample. Finally, the subject invention provides a method for typing Mycobacteria in a clinical sample containing Mycobacteria.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 6 OF 8 USPATFULL
AN 96:65466 USPATFULL
TI In situ **polymerase chain reaction**
IN Nuovo, Gerard J., Calverton, NY, United States
Bloch, Will, El Cerrito, CA, United States
PA Hoffmann-La Roche Inc., Nutley, NJ, United States (U.S. corporation)
Research Foundation of State of New York, Albany, NY, United States (U.S. corporation)
PI US 5538871 19960723
AI US 1995-390256 19950217 (8)
RLI Continuation of Ser. No. US 1991-733419, filed on 23 Jul 1991, now abandoned
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Sisson, Bradley L.
LREP Gould, George M.; Tramaloni, Dennis P.; Sias, Stacey R.
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1351
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Improvements to the in situ polymerase chain reaction (PCR), a process of in vitro enzymatic amplification of specific nucleic acid sequences within the cells where they originate, can be achieved by changing the way that the enzymatic reaction is started. Reaction initiation is delayed until the start of PCR thermal cycling, either by withholding a subset of PCR reagents from the cellular preparation until the preparation has been heated to 50.degree. C. to 80.degree. C., immediately before thermal cycling is begun, or by adding to the PCR reagents a single-stranded DNA binding protein which blocks reaction at temperatures below about 50.degree. C. If the in situ PCR is performed on cellular preparations already attached to a microscope slide, thermal

compartment designed optimally to hold the microscope slide and any vapor barrier covering the slide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 7 OF 8 USPATFULL
AN 96:36463 USPATFULL
TI Enzymatic inverse **polymerase chain reaction** library mutagenesis
IN Stemmer, Willem P. C., Carlsbad, CA, United States
PA Eli Lilly and Company, Indianapolis, IN, United States (U.S. corporation)
PI US 5512463 19960430
AI US 1994-252057 19940601 (8)
DCD 20140119
RLI Continuation of Ser. No. US 1991-806154, filed on 12 Dec 1991, now abandoned which is a continuation-in-part of Ser. No. US 1991-691140, filed on 26 Apr 1991, now abandoned
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Arthur, Lisa
LREP Knobbe, Martens, Olson & Bear
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1950
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention discloses a method for generating a recombinant library by introducing one or more changes within a predetermined region of double-stranded nucleic acid, comprising providing a first primer population and a second primer population, each of the populations having a variable base composition at known positions along the primers,
the primers incorporating a class IIS restriction enzyme recognition sequence, being capable of directing change in the nucleic acid sequence
and being substantially complementary to the double stranded nucleic acid to permit hybridization thereto. The method additionally comprises hybridizing the first and second primer populations to opposite strands of the double stranded nucleic acid to form a first pair of primer-templates oriented in opposite directions, performing enzymatic inverse polymerase chain reaction to generate at least one linear copy of the double stranded nucleic acid incorporating the change directed by
the primers, cutting the double stranded nucleic acid copy with a class IIS restriction enzyme to form a restricted linear nucleic acid molecule
containing the change, joining termini of the restricted linear nucleic acid molecule to produce double-stranded circular nucleic acid and introducing the nucleic acid into compatible host cells. A method is additionally provided for generating a recombinant library using wobble-base mutagenesis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 8 OF 8 USPATFULL
AN 96:12945 USPATFULL
TI **PCR** primers for detection of legionella species and methods for controlling visual intensity in hybridization assays
IN Picone, Teresa K. H., Benicia, CA, United States
McCallum, Theresa M., Pleasant Hill, CA, United States
Zoccoli, Michael A., Moraga, CA, United States
PA Hoffmann-La Roche Inc., Nutley, NJ, United States (U.S. corporation)
PI US 5491225 19960213
WO 9211273 19920709

WO 1991-US9688 19911219
19930527 PCT 371 date
19930527 PCT 102(e) date
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Sisson, Bradley L.
LREP Gould, George M.; Sias, Stacey R.; Petry, Douglas A.
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1301
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides for superior nucleic acid primers for amplification of select target regions of the genome of the genus Legionella. The invention facilitates detection of pathogenic and nonpathogenic forms of this genus. The invention further provides for processes for using the primers in template dependent nucleic acid polymerase extension reactions to amplify select target regions. Kits for the use of these primers are also provided. This invention further provides for methods of controlling the intensity of visual signal for detection of duplex formation in nucleic acid hybridization assays under high stringent conditions. This method involves the blending of different capture probes onto a solid support.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l4 1 kwic

L4 ANSWER 1 OF 8 USPATFULL
TI Salmonella identification by the **polymerase chain reaction**
SUMM . . . of detection have recently proliferated and are available for detection of DNA or RNA from the target organism. A useful **review** is found in the article by M. J. Wolcott in J. Food Protection 54, (5), pp. 387-401, 1991, Typical techniques. . .
SUMM . . . altered backbone chains such as PNA where the ribose units of the backbone are replaced by other units such as **amino acids** or peptides but the sequence of bases is retained and the molecule hybridises in the same way as the said. . .

=> d l4 6 kwic

L4 ANSWER 6 OF 8 USPATFULL
TI In situ **polymerase chain reaction**
SUMM . . . the fields of genetics, molecular biology, cellular biology, clinical chemistry, forensic science, and analytical biochemistry, as described in the following **review** volumes and articles: Erlich (ed.), 1989, PCR Technology, Stockton Press (New York); Erlich et al. (eds.), 1989, Polymerase Chain Reaction,. . .
SUMM . . . 86:1193-1197). SSBs possess enough structural similarity to suggest that DNA binding is associated with a consensus structure of alternating aromatic **amino acids** (phenylalanine, tyrosine, and tryptophan) and charged **amino acids** (glutamate, aspartate, lysine, and arginine) (Prasad and Chiu, 1987, J. Mol. Biol. 193:579-584) such that artificial polypeptides might be created. . .
SUMM . . . nucleic acid hybridization methods have evolved to detect target sequences in the cells or organelles where they originated (for a

6:366-379). Typically, in situ hybridization entails (1) preparation of.

. .

ETD . . . 16 genome per human genome, were grown to density of about 10.sup.5 cells/mL in Eagle's minimal essential medium with non-essential

amino acids, sodium pyruvate, and 15% fetal bovine serum, washed two times in Tris-buffered saline, adjusted to an approximate density of 10.sup.4. . .

=> d his

(FILE 'HOME' ENTERED AT 06:33:32 ON 21 NOV 2000)

FILE 'BIOSIS, MEDLINE, WPIDS, USPATFULL' ENTERED AT 06:33:43 ON 21 NOV 2000

L1 5642 S (PCR OR POLYMERASE CHAIN REACTION) AND REVIEW
L2 347 S (PCR OR POLYMERASE CHAIN REACTION)/TI AND REVIEW
L3 8 S L2 AND AMINO ACID?
L4 8 DUP REM L3 (0 DUPLICATES REMOVED)

=> s l4 and proline

L5 0 L4 AND PROLINE

=> 's l4 and glycine

'S IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s l4 and glycine

L6 1 L4 AND GLYCINE

=> d l6 bib abs

L6 ANSWER 1 OF 1 USPATFULL
AN 1998:134819 USPATFULL
TI In situ recombinant **PCR** within single cells
IN Embleton, Michael J., Nottingham, United Kingdom
Gorochov, Guy, Cambridge, United Kingdom
Jones, Peter T., Cambridge, United Kingdom
Winter, Gregory P., Cambridge, United Kingdom
PA Medical Research Council, England (non-U.S. corporation)
PI US 5830663 19981103
WO 9303151 19930218
AI US 1994-190199 19940713 (8)
WO 1992-GB1483 19920810
19940713 PCT 371 date
19940713 PCT 102(e) date
PRAI GB 1991-17352 19910810
GB 1992-12419 19920611
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Fredman, Jeffrey
LREP Cushman Darby & Cushman IP Group of Pillsbury Madison & Sutro
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 19 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 1925

AB Disclosed is a method of treating a heterogeneous population of cells
to
link together copies of two or more nucleic acid sequences from at
least
some of the cells, the arrangement being such that copies of the DNA sequences from an individual cell are preferentially linked in the vicinity of the nucleic acid from which the copies are derived. Also disclosed are recombinant proteins expressed by the method of the invention and kits for performing said method.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l6 kwic

L6 ANSWER 1 OF 1 USPATFULL
TI In situ recombinant **PCR** within single cells
SUMM . . . either associated non-covalently, or via disulphide bonds or via a peptide linker. The antigen binding domains are more variable in **amino acid** sequence than the other domains of the antibody, and are therefore termed variable (V) domains in contrast to the constant. . .
SUMM . . . technology have been proposed for making antibodies from B-lymphocytes (see Milstein and winter, Nature 349, 293-299 (1991) (reference 11) for **review** and references). The key step is the cloning of the genes encoding the VH and VL genes directly from B-lymphocytes. . .
SUMM . . . is possible that some artificial combinations with binding activities may be similar to the original combination, perhaps with a few **amino acid** substitutions. Nevertheless it is expected that the majority of such artificial antibodies will have
lower
affinities than the original combination. . .
DETD . . . 4 more times in 1 ml ice-cold PBS, with vigorous pipetting,
and
suspended in 0.2-0.5 ml cold PBS containing 0.1M **glycine**. A sample was examined microscopically in a haemocytometer, and if clumps were present they were dispersed into single cells by. . . through a 26 gauge hypodermic needle. The cells were then counted and adjusted to 10.sup.7 per ml in PBS +0.1M **glycine**, and aliquoted into 0.5 ml tubes (usually 0.05-0.1 ml per tube) and frozen in dry ice. The frozen aliquots were. . .
DETD . . . ul
Forward Link primer 0.5 ul
Back Link primer 0.5 ul
dNTPs (5 mM) 2.0 ul
10 .times. PCR buffer
5.0 ul
Cell template (in PBS/**glycine**)
10.0 ul
Taq polymerase (5 units/ul)
0.5 ul

DETD . . . away, leaving the cells at the bottom of the well. The cells were then suspended in 0.2 ml of PBS/0.1M **glycine** and spun down in a microfuge at 13,000 rpm. After resuspension in the same
buffer
they were again spun down for a 2nd wash, then resuspended in 10 .mu.l PBS/**glycine** for use as the 2nd stage template. Tubes from the BioOven were spun at 13,000 rpm and the supernatant PCR mix removed,
and
the cells washed twice in 0.2 ml PBS/**glycine**, before final resuspension in 10 ul PBS/**glycine** for use as 2nd stage

DETD . . . were again washed 3 times in ice-cold PBS with vigorous pipetting. A final wash was given in PBS containing 0.1M **glycine**, and the cells were resuspended in 0.2 to 0.5 ml of the same buffer, using a 1 ml syringe and. . .

DETD . . . 42.degree. C. for 1 hour, then the cells were spun down, washed in 200 ul PBS (pH 7.2) containing 0.1M **glycine** (PBS/0.1M **glycine**) and resuspended in 20 ul of the same buffer for use immediately in PCR. For K562 cells, cDNA synthesis was. . .

DETD . . . set up in 50 ul volumes in 0.5 ml Sarstedt tubes with 10 ul fixed template cells in PBS/0.1 M **glycine** buffer, 25 pmol back primer, 25 pmol forward primer, 200 uM dNTPs, 5 ul 10.times. Taq polymerase buffer (Promega) and. . .

DETD . . . sequence, 200 uM dNTPs, 5 ul 10.times.Taq polymerase buffer, 2.5 units Taq polymerase, and 10 ul fixed cells in PBS/0.1M **glycine** buffer. Generally 10 (but sometimes up to 5.times.10.sup.5) cells per tube were used, and the tubes were given 30 cycles. . . and 72.degree. C. for 30 secs. The cells were spun down at 13,000 rpm, washed twice in 200 ul PBS/0.1M **glycine**, and resuspended in 10 ul PBS/**glycine**. To amplify the assembled products, a second PCR was set up with the washed cells, nested primers (23) using 25. . .

DETD . . . (NQ10) fixed cells using the primers MOLFOR, MOJH3FOR, B1-8LFOR and B1-8VHLINK3, and the cells washed and resuspended in PBS/0.1 M **glycine** for PCR assembly. The first PCR was carried out using the VL forward primers MOLFOR and B1-8LFOR and the VH. . .

DETD . . . the hybridoma and leukaemia cells with formal saline, permeabilised them with NP40, and stored the cells frozen in PBS/0.1 M **glycine**. We found that with these cells, our method resulted in high yields of amplified DNA as detected in the cell. . .

DETD Consistently higher yields of amplified DNA were obtained when cells were added to the reaction in their storage buffer (PBS/0.1M **glycine**) rather than water. In NQ10 cells subjected to two-stage PCR assembly in which 10 uCi (25 pmol) .sup.35 S-dATP was. . .

DETD . . . Nonidet P40 (BDH) in water. After a further 3 washes in PBS the cells were suspended in PBS containing 0.1M **glycine** and counted. They were stored frozen at -70.degree. C.

DETD . . . the whole mixture incubated at 42.degree. C. for 1 hour. The cells were then spun down, washed once in PBS/0.1M **glycine** and resuspended in the same buffer for PCR.

DETD The cells were spun down and washed twice in PBS/0.1M **glycine**, and suspended in 10 .mu.l of this buffer for a 2nd PCR together with the following mix:

DETD (2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 **amino acids**

(B) TYPE: **amino acid**

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGln
151015
SerLeuSerIleThrCysThrValSerGlyPheSerLeuThrSerTyr
202530
GlyValHisTrpValArgGlnProProGlyLysGlyLeuGluTrpLeu
354045
GlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeuMet
505560
SerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu
65707580
LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAla

ArgAspArgGlyAlaTyrTrpGlyGlnGlyThrLeuValThrValSer
100105110
AlaGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySer
115120125
GlnIleValLeuThrGlnSerProAlaIleMetSerAlaSerProGly
130135140
GlnLysValThrMetThrCysSerAlaSerSerSerValSerTyrMet
145150155160
HisTrpTyrGlnGlnLysSerGlyThrSerProLysArgTrpIleTyr
165170175
AspThrSerLysLeuAlaSerGlyValProAlaArgPheSerGlySer
180185190
GlySerAlaThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu
195200205
AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThr
210215220
PheGlyAlaGlyThrLysLeuGluLeuLysArg
225230235

DETD (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 **amino acids**
(B) TYPE: **amino acid**
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AspValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGly
151015
SerArgLysLeuSerCysAlaAlaSerGlyPheThrPheSerSerPhe
202530
GlyMetHisTrpValArgGlnAlaProGluLysGlyLeuGluTrpVal
354045
AlaTyrIleSerSerGlySerSerThrIleTyrTyrAlaAspThrVal
505560
LysGlyArgPheThrIleSerArgAspAsnProLysAsnThrLeuPhe
65707580
LeuGlnMetThrSerLeuArgSerGluAspThrAlaMetTyrTyrCys
859095
AlaArgAspTyrGlyAlaTyrTrpGlyGlnGlyThrLeuValThrVal
100105110
SerAlaAlaSerGlnIleValLeuThrGlnSerProAlaIleMetSer
115120125
AlaSerProGlyGluLysValThrMetThrCysSerAlaSerSerSer
130135140
ValArgTyrMetAsnTrpPheGlnGlnLysSerGlyThrSerProLys
145150155160
ArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg
165170175
PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSer
180185190
MetGluAlaGluAspAlaAlaThrTyrTyrCysGlnGlnTrpSerSer
195200205
AsnProLeuThrPheGlyAlaGlyThrLysLeuGluLeuLysArg
210215220

DETD (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 **amino acids**
(B) TYPE: **amino acid**
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AspValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGly
151015
SerArgLysLeuSerCysAlaAlaSerGlyPheThrPheSerSerPhe
202530

354045
AlaTyrIleSerSerGlySerSerThrIleTyrTyrAlaAspThrVal
505560
LysGlyArgPheThrIleSerArgAspAsnProLysAsnThrLeuPhe
65707580
LeuGlnMetThrSerLeuArgSerGluAspThrAlaMetTyrTyrCys
859095
AlaArgAspTyrGlyAlaTyrTrpGlyGlnGlyThrLeuValThrVal
100105110
SerAlaGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGly
115120125
SerGlnIleValLeuThrGlnSerProAlaIleMetSerAlaSerPro
130135140
GlyGluLysValThrMetThrCysSerAlaSerSerSerValArgTyr
145150155160
MetAsnTrpPheGlnGlnLysSerGlyThrSerProLysArgTrpIle
165170175
TyrAspThrSerLysLeuSerSerGlyValProAlaArgPheSerGly
180185190
SerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAla
195200205
GluAspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeu
210215220
ThrPheGlyAlaGlyThrLysLeuGluLeuLysArg
225230235

DETD (2) INFORMATION FOR SEQ ID NO:67:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 **amino acids**
(B) TYPE: **amino acid**
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGln
151015
SerLeuSerIleThrCysThrValSerGlyPheSerLeuThrSerTyr
202530
GlyValHisTrpValArgGlnProProGlyLysGlyLeuGluTrpLeu
354045
GlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeuMet
505560
SerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu
65707580
LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAla
859095
ArgAspArgGlyAlaTyrTrpGlyGlnGlyThrLeuValThrValSer
100105110
AlaAlaSerGlnIleValLeuThrGlnSerProAlaIleMetSerAla
115120125
SerProGlyGlnLysValThrMetThrCysSerAlaSerSerSerVal
130135140
SerTyrMetHisTrpTyrGlnGlnLysSerGlyThrSerProLysArg
145150155160
TrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe
165170175
SerGlySerGlySerAlaThrSerTyrSerLeuThrIleSerSerMet
180185190
GluAlaGluAspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsn
195200205
ProLeuThrPheGlyAlaGlyThrLysLeuGluLeuLysArg
210215220

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(FILE 'HOME' ENTERED AT 06:33:32 ON 21 NOV 2000)

FILE 'BIOSIS, MEDLINE, WPIDS, USPATFULL' ENTERED AT 06:33:43 ON 21 NOV 2000

L1 5642 S (PCR OR POLYMERASE CHAIN REACTION) AND REVIEW
L2 347 S (PCR OR POLYMERASE CHAIN REACTION)/TI AND REVIEW
L3 8 S L2 AND AMINO ACID?
L4 8 DUP REM L3 (0 DUPLICATES REMOVED)
L5 0 S L4 AND PROLINE
L6 1 S L4 AND GLYCINE

=> s polymerase same proline

L7 0 POLYMERASE SAME PROLINE

=> s polymerase same glycine

L8 0 POLYMERASE SAME GLYCINE

=> s polymerase same amino acid?

L9 0 POLYMERASE SAME AMINO ACID?

=> s polymerase (20a) amino acid?

L10 6850 POLYMERASE (20A) AMINO ACID?

=> s polymerase (10a) amino acid?

L11 3427 POLYMERASE (10A) AMINO ACID?

=> s polymerase (5a) AMINO ACID?

L12 1569 POLYMERASE (5A) AMINO ACID?

=> S POLYMERASE (3A) AMINO ACID?

L13 823 POLYMERASE (3A) AMINO ACID?

=> D L13 BIB ABS KWIC 1-5

L13 ANSWER 1 OF 823 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:490047 BIOSIS
DN PREV200000490168
TI Structural study of the N-terminal domain of the alpha subunit of Escherichia coli RNA polymerase solubilized with non-denaturing detergents.
AU Otomo, Takanori; Yamazaki, Toshio; Murakami, Katsuhiko; Ishihama, Akira; Kyogoku, Yoshimasa (1)
CS (1) Fukui Institute of Technology, 3-6-1 Gakuen, Fukui, 910-8505 Japan
SO Journal of Biochemistry (Tokyo), (Aug., 2000) Vol. 128, No. 2, pp. 337-344. print.
ISSN: 0021-924X.
DT Article
LA English
SL English
AB The amino-terminal domain of the alpha subunit (alphaNTD) of Escherichia coli RNA **polymerase** consisting of 235 **amino acid** residues functions in the assembly of the alpha, beta, and beta' subunits into the core-enzyme. It has a tendency to form aggregates by itself at higher concentrations. For NMR structural analysis of alphaNTD, the solution conditions, including the use of non-denaturing detergents, were optimized by monitoring the translational diffusion

conditions with taurodeoxycholate and with the aid of deuteration of the sample, alphaNTD gave triple-resonance spectra of good quality, which allowed the assignment of a large part of the backbone resonances. Analysis of the pattern of NOEs observed between the backbone amide and alpha-protons demonstrated that alphaNTD has three alpha-helices and two beta-sheets. Although the secondary structure elements essentially coincide with those in the crystal structure, the larger of the two beta-sheets has two additional beta-strands. The irregular NOE patterns observed for the three positions in the beta-sheets suggest the presence of beta-bulge structures. The positions of the three helices coincide with the conserved sequence regions that are responsible for the subunit assembly.

AB The amino-terminal domain of the alpha subunit (alphaNTD) of Escherichia coli RNA **polymerase** consisting of 235 **amino acid** residues functions in the assembly of the alpha, beta, and beta' subunits into the core-enzyme. It has a tendency to. . .

L13 ANSWER 2 OF 823 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:466776 BIOSIS
DN PREV200000466776
TI Iridovirus homologues of cellular genes: Implications for the molecular evolution of large DNA viruses.
AU Tidona, Christian A. (1); Darai, Gholamreza (1)
CS (1) Institut fuer Medizinische Virologie, Universitaet Heidelberg, Im Neuenheimer Feld 324, D-69120, Heidelberg Germany
SO Virus Genes, (August, 2000) Vol. 21, No. 1-2, pp. 77-81. print. ISSN: 0920-8569.
DT General Review
LA English
SL English
AB Iridoviruses belong to the group of large cytoplasmic deoxyriboviruses and infect either insects or vertebrates. In analogy to other large DNA viruses of eucaryotes it was found that iridoviruses encode a number of cellular protein homologues. The majority of these proteins represent orthologues of cellular enzymes involved in transcription, replication and nucleotide metabolism. Others may have the potential to interfere with cell cycle regulation or immune defence mechanisms of the host. This raises the question about the phylogenetic origin of the corresponding viral genes. During the evolution of large cytoplasmic DNA viruses such as iridoviruses, poxviruses, and African swine fever virus the acquirement of cellular genes appears to be a crucial event. Each member of this group of viruses encodes a DNA polymerase, two subunits of the DNA-dependent RNA polymerase, and two subunits of the ribonucleotide reductase. It is important to note that all of these viral proteins show a high level of multidomain structure conservation as compared to their cellular orthologues. As a consequence the large cytoplasmic DNA viruses have the ability to replicate independently of the cellular nucleus in the cytoplasm of the infected cell. Assuming a common cellular origin o f viral DNA **polymerase** genes the corresponding **amino acid** sequences were chosen to construct a phylogenetic tree showing the relatedness among large DNA viruses of eucaryotes.

AB. . . of the cellular nucleus in the cytoplasm of the infected cell. Assuming a common cellular origin o f viral DNA **polymerase** genes the corresponding **amino acid** sequences were chosen to construct a phylogenetic tree showing the relatedness among large DNA viruses of eucaryotes.

L13 ANSWER 3 OF 823 BIOSIS COPYRIGHT 2000 BIOSIS

DN PREV200000452895
TI Hydrophobic interactions in the hinge domain of DNA polymerase beta are important but not sufficient for maintaining fidelity of DNA synthesis.
AU Opresko, Patricia L.; Shiman, Ross; Eckert, Kristin A. (1)
CS (1) Department of Biochemistry and Molecular Biology, Jake Gittlen Cancer Research Institute, Pennsylvania State University College of Medicine, M. S. Hershey Medical Center, Hershey, PA, 17033 USA
SO Biochemistry, (September 19, 2000) Vol. 39, No. 37, pp. 11399-11407. print.
ISSN: 0006-2960.
DT Article
LA English
SL English
AB We previously described a general mutator form of mammalian DNA polymerase beta containing a cysteine substitution for tyrosine 265. Residue 265 localizes to a hydrophobic hinge region predicted to mediate a polymerase conformational change that may aid in nucleotide selectivity. In this study we tested the hypothesis that van der Waals and hydrophobic contacts between Y265 and neighboring residues are important for DNA synthesis fidelity and catalysis, by altering interactions in the hinge domain via substitution at position 265. Consistent with the importance of hydrophobic interactions, we found that phenylalanine, leucine, and tryptophan substitutions did not alter significantly the steady-state catalytic efficiency of DNA synthesis, relative to wild type, while the polar serine substitution decreased catalytic efficiency 6-fold. However, we found that all substitutions other than phenylalanine increased the error frequency, relative to wild type, in the order serine > tryptophan = leucine. Therefore, maintenance of the hydrophobicity of residue 265 was not sufficient for maintaining fidelity of DNA synthesis. We conclude that while hydrophobic interactions in the hinge domain are important for fidelity, additional factors such as electrostatic and van der Waals interactions contributed by the tyrosine 265 aromatic ring are required to retain wild-type fidelity.
IT . . .
Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA: catalysis, synthesis fidelity; DNA **polymerase** beta: **amino acid** substitution, hinge domain, hydrophobic interactions

L13 ANSWER 4 OF 823 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:388446 BIOSIS
DN PREV200000388446
TI Partial sequence of porcine reproductive and respiratory syndrome virus strain VR-2402 ORF1b.
AU Petermann, S. R. (1); Rybolt, R. A. (1); Doetkott, D. M. (1); Berry, E. S. (1); Rust, L. (1)
CS (1) North Dakota State Univ., Fargo, ND USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 637. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology Los Angeles, California, USA May 21-25, 2000 American Society for Microbiology
. ISSN: 1060-2011.
DT Conference

SL English
IT Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
RNA; RNA-dependent RNA **polymerase**: **amino acid** sequence, analysis; amino acids; enzymes; oligonucleotides; proteins

L13 ANSWER 5 OF 823 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:382668 BIOSIS
DN PREV200000382668
TI The role of steric hindrance in 3TC resistance of human immunodeficiency virus type-1 reverse transcriptase.
AU Gao, Hong-Qiang; Boyer, Paul L.; Sarafianos, Stefan G.; Arnold, Edward; Hughes, Stephen H. (1)
CS (1) HIV Drug Resistance Program, National Cancer Institute-FCRDC, Building 539, Room 130A, Frederick, MD, 21702-1201 USA
SO Journal of Molecular Biology, (7 July, 2000) Vol. 300, No. 2, pp. 403-419.
print.
ISSN: 0022-2836.
DT Article
LA English
SL English
AB Treating HIV infections with drugs that block viral replication selects for drug-resistant strains of the virus. Particular inhibitors select characteristic resistance mutations. In the case of the nucleoside analogs 3TC and FTC, resistant viruses are selected with mutations at amino acid residue 184 of reverse transcriptase (RT). The initial change is usually to M184I; this virus is rapidly replaced by a variant carrying the mutation M184V. 3TC and FTC are taken up by cells and converted into 3TCTP and FTCTP. The triphosphate forms of these nucleoside analogs are incorporated into DNA by HIV-1 RT and act as chain terminators. Both of the mutations, M184I and M184V, provide very high levels of resistance in vivo; purified HIV-1 RT carrying M184V and M184I also shows resistance to 3TCTP and FTCTP in in vitro **polymerase** assays. **Amino acid** M184 is part of the dNTP binding site of HIV-1 RT. Structural studies suggest that the mechanism of resistance of HIV-1 RTs carrying the M184V or M184I mutation involves steric hindrance, which could either completely block the binding of 3TCTP and FTCTP or allow binding of these nucleoside triphosphate molecules but only in a configuration that would prevent incorporation. The available kinetic data are ambiguous: one group has reported that the primary effect of the mutations is at the level of 3TCTP binding; another, at the level of incorporation. We have approached this problem using assays that monitor the ability of HIV-1 RT to undergo a conformational change upon binding a dNTP. These studies show that both wild-type RT and the drug-resistant variants can bind 3TCTP at the polymerase active site; however, the binding to M184V and M184I is somewhat weaker and is sensitive to salt. We propose that the drug-resistant variants bind 3TCTP in a strained configuration that is salt-sensitive and is not catalytically competent.
AB. . . resistance in vivo; purified HIV-1 RT carrying M184V and M184I also shows resistance to 3TCTP and FTCTP in in vitro **polymerase** assays. **Amino acid** M184 is part of the dNTP binding site of HIV-1 RT. Structural studies suggest that the mechanism of resistance of. . .

(FILE 'HOME' ENTERED AT 06:33:32 ON 21 NOV 2000)

FILE 'BIOSIS, MEDLINE, WPIDS, USPATFULL' ENTERED AT 06:33:43 ON 21 NOV 2000

L1	5642	S (PCR OR POLYMERASE CHAIN REACTION) AND REVIEW
L2	347	S (PCR OR POLYMERASE CHAIN REACTION)/TI AND REVIEW
L3	8	S L2 AND AMINO ACID?
L4	8	DUP REM L3 (0 DUPLICATES REMOVED)
L5	0	S L4 AND PROLINE
L6	1	S L4 AND GLYCINE
L7	0	S POLYMERASE SAME PROLINE
L8	0	S POLYMERASE SAME GLYCINE
L9	0	S POLYMERASE SAME AMINO ACID?
L10	6850	S POLYMERASE (20A) AMINO ACID?
L11	3427	S POLYMERASE (10A) AMINO ACID?
L12	1569	S POLYMERASE (5A) AMINO ACID?
L13	823	S POLYMERASE (3A) AMINO ACID?

Search Results -

Term	Documents
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COMPSNS.USPT.	37
COMPOSITIONS.USPT.	305090
PCR.USPT.	16963
PCRS.USPT.	535
AMINO.USPT.	187262
AMINOES.USPT.	1
AMINOS.USPT.	296
AMINOE.USPT.	45
(L4 AND COMPOSITION SAME PCR SAME AMINO ACID).USPT.	25

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USPT	l2 same nucleic adj acid	1556	L4
USPT	l2 and nucleic adj acid	5288	L3
USPT	pcr same amino adj acid	5497	L2
USPT	6110900.pn. and amino adj acid	1	L1

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1. Document ID: US 6135941 A

L5: Entry 1 of 25 File: USPT Oct 24, 2000

US-PAT-NO: 6135941
DOCUMENT-IDENTIFIER: US 6135941 A
TITLE: Human immune system associated molecules

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

2. Document ID: US 6130045 A

L5: Entry 2 of 25 File: USPT Oct 10, 2000

US-PAT-NO: 6130045
DOCUMENT-IDENTIFIER: US 6130045 A
TITLE: Thermostable polymerase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

3. Document ID: US 6130077 A

L5: Entry 3 of 25 File: USPT Oct 10, 2000

US-PAT-NO: 6130077
DOCUMENT-IDENTIFIER: US 6130077 A
TITLE: Human cytochrome P450

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

4. Document ID: US 6069229 A

L5: Entry 4 of 25 File: USPT May 30, 2000

US-PAT-NO: 6069229
DOCUMENT-IDENTIFIER: US 6069229 A
TITLE: Mammalian proteinases; oxidoreductases; related reagents

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

5. Document ID: US 6030835 A

L5: Entry 5 of 25 File: USPT Feb 29, 2000

US-PAT-NO: 6030835
DOCUMENT-IDENTIFIER: US 6030835 A
TITLE: Methods and composition for identifying group a streptococcus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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6. Document ID: US 6025465 A

L5: Entry 6 of 25 File: USPT Feb 15, 2000

US-PAT-NO: 6025465
DOCUMENT-IDENTIFIER: US 6025465 A
TITLE: Insulin-like growth factor binding protein (IGFBP-6)

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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7. Document ID: US 5981259 A

L5: Entry 7 of 25 File: USPT Nov 9, 1999

US-PAT-NO: 5981259
DOCUMENT-IDENTIFIER: US 5981259 A
TITLE: CD4+ T-lymphocyte protease genes and inhibitors thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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8. Document ID: US 5968744 A

L5: Entry 8 of 25 File: USPT Oct 19, 1999

US-PAT-NO: 5968744
DOCUMENT-IDENTIFIER: US 5968744 A
TITLE: Human cornichon molecule

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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9. Document ID: US 5928874 A

L5: Entry 9 of 25 File: USPT Jul 27, 1999

US-PAT-NO: 5928874
DOCUMENT-IDENTIFIER: US 5928874 A
TITLE: Nek1-related protein kinase

10. Document ID: US 5922595 A

L5: Entry 10 of 25 File: USPT Jul 13, 1999

US-PAT-NO: 5922595
DOCUMENT-IDENTIFIER: US 5922595 A
TITLE: Cyclic GMP phosphodiesterase

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Term	Documents
COMPOSITION.USPT.	502050
COMPSN.USPT.	162
COMPSNS.USPT.	37
COMPOSITIONS.USPT.	305090
PCR.USPT.	16963
PCRS.USPT.	535
AMINO.USPT.	187262
AMINOES.USPT.	1
AMINOS.USPT.	296
AMINOE.USPT.	45
(L4 AND COMPOSITION SAME PCR SAME AMINO ACID).USPT.	25

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